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Ecological stress and adaptive genetic evolution in plant populations at global, regional, and local scales

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The genomic revolution has dramatically opened wide horizons for evolutionary studies, linking molecular and organismal organizational levels. Here, I primarily review the 1975-2000 research program in the Institute of Evolution, University of Haifa (Nevo, 2001). This program involves biodiversity evolution, from bacteria to mammals, *genes, genomes, phenomes, populations, species, ecosystems,* and *biota* and their intimate reciprocal interaction with the spatiotemporal variables, and stressful physical and biotic environments resulting in *adaptation* and *speciation.*

Our model organisms represent diverse taxa across life, from bacteria to mammals, in an attempt to unravel regularity, convergence, and divergence of genotypic and phenotypic patterns: *Nostoc linckia* (cyanobacterium); *Sordaria fimicola* (coprophilous fungus); *Triticum dicoccoides* and *Hordeum spontaneum* (wild cereals); *Drosophila melanogaster* (fruit fly), *Spalax ehrenbergi* superspecies (subterranean mole rats); *Acomys cahirinus* and *Apodemus mystacinus* (aboveground rodents). We also *globally* and *regionally* studied the population genetics of 1200 species from bacteria to mammals, primarily based on literature data and species richness of 3000 species in the two "Evolution Canyons".

Summary of Evidence

The evidence across life, involving numerous species, populations and individuals, displays massive genetic polymorphic correlations and parallelisms to environmental heterogeneity and stress. Generally, *genome* and *phenome* diversity are *nonrandom* and correlated with stress and higher environmental heterogeneity or niche-width. Genetic diversity is partly correlated with, and predictable by, a few ecological (primarily climatic) variables. These correlations largely characterize *global, regional,* and *local scales.*

Conclusions

The enigma of genetic diversity and *genome-phenome* organization and evolution in nature has been fruitfully explored using modern molecular techniques. Genotypic and phenotypic diversity has been found in all species at the protein, DNA, and organismal levels. Genome-phenome organization in nature is *nonrandom, heavily structured, and correlated with abiotic and environmental diversity and stress.* Deciphering the origin and maintenance of genetic diversity will be enhanced through investigations focusing on the interface between *ecology* and *genomics.* Critical tests and strong inferences in nature of abiotic and biotic factors include transplant experiments at microscales and macroscales (Nevo 1998, 2001), to unravel genome organization and fitness in contrasting and changing environments and to relate *genomics* to *phenomics.*

Reassuringly, DNA polymorphisms (RFLPs, RADPs, AFLPs, SSRs, SNPs) and the *noncoding* genome largely mirror protein (isozyme) polymorphisms, are subjected to natural selection, and can be utilized to highlight genome structure and evolution. The focus of evolutionary biology is the organism-environment interaction involving genomes, phenomes and biomes, across the tree of life. The *noncoding* and regulatory *genome* should become a central target in understanding evolution.

Nevo, E. 1998. Molecular evolution and ecological stress at global, regional and local scales: The Israeli perspective. J. Exp. Zool. 282:95-119.

Nevo, E. 2001. Evolution of genome-phenome diversity under environmental stress. PNAS 98:6233-6240.